

5021US_SEQ.TXT

SEQUENCE LISTING

<110> Cowan, Conrad L.

<120> METHODS OF SCREENING COMPOSITIONS FOR G PROTEIN-COUPLED RECEPTOR AGONIST ACTIVITY

<130> 067437-5021-US

<140> US 10/572,529

<141> 2007-03-05

<150> PCT/US2004/030261

<151> 2004-09-16

<150> US 60/503,447

<151> 2003-09-16

<160> 59

<170> FastSEQ for Windows version 4.0

<210> 1

<211> 43

<212> PRT

<213> Homo sapiens

<400> 1

Asn	Pro	Ile	Val	Tyr	Ala	Phe	Arg	Ile	Gln	Lys	Phe	Arg	Val	Thr	Phe
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Leu	Lys	Ile	Trp	Asn	Asp	His	Phe	Arg	Cys	Gln	Pro	Ala	Pro	Pro	Ile
							20'		25				30		
Asp	Glu	Asp	Leu	Pro	Glu	Glu	Arg	Pro	Asp	Asp					
							35		40						

<210> 2

<211> 177

<212> PRT

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<400> 2

Asn	Pro	Ile	Ile	Tyr	Pro	Cys	Ser	Ser	Lys	Glu	Phe	Lys	Arg	Ala	Phe
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Val	Arg	Ile	Leu	Gly	Cys	Gln	Cys	Arg	Gly	Arg	Gly	Arg	Arg	Arg	
								20'	25			30			
Arg	Arg	Arg	Arg	Leu	Gly	Gly	Cys	Ala	Tyr	Thr	Tyr	Arg	Pro	Trp	
								35	40		45				
Thr	Arg	Gly	Gly	Ser	Leu	Glu	Arg	Ser	Gln	Ser	Arg	Lys	Asp	Ser	
								50	55		60				
Asp	Asp	Ser	Gly	Ser	Cys	Leu	Ser	Gly	Ser	Gln	Arg	Thr	Leu	Pro	
								65	70		75		80		
Ala	Ser	Pro	Ser	Pro	Gly	Tyr	Leu	Gly	Arg	Gly	Ala	Pro	Pro	Val	
								85	90		95				
Glu	Leu	Cys	Ala	Phe	Pro	Glu	Trp	Lys	Ala	Pro	Gly	Ala	Leu	Ser	
								100	105		110				
Leu	Pro	Ala	Pro	Glu	Pro	Pro	Gly	Arg	Arg	Gly	Arg	His	Asp	Ser	
								115	120		125				
Pro	Leu	Phe	Thr	Phe	Lys	Leu	Leu	Thr	Glu	Pro	Glu	Ser	Pro	Gly	
								130	135		140				
Asp	Gly	Gly	Ala	Ser	Asn	Gly	Gly	Cys	Glu	Ala	Ala	Ala	Asp	Val	

5021US_SEQ.TXT

145 Asn Gly Gln Pro Gly Phe Lys Ser Asn Met Pro Leu Ala Pro Gly Gln
 150 165 170 175
 Phe

<210> 3
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<400> 3
 Asn Pro Val Ile Tyr Thr Ile Phe Asn His Asp Phe Arg Arg Ala Phe
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 Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys Arg Ile Val
 20 25

<210> 4
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<400> 4
 Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg Ala Phe
 1 5 10 15
 Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
 20 25

<210> 5
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<400> 5
 Asn Pro Val Ile Tyr Thr Val Phe Asn Gln Asp Phe Arg Pro Ser Phe
 1 5 10 15
 Lys His Ile Leu Phe Arg Arg Arg Arg Gly Phe Arg Gln
 20 25 30

<210> 6
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<400> 6
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 1 5 10 15
 Gly Leu Leu Cys Cys Ala Arg Arg Ala Ala Arg Arg Arg His Ala Thr
 20 25 30
 His Gly Asp Arg Pro Arg Ala Ser Gly Cys Leu Ala Arg Pro Gly Pro
 35 40 45
 Pro Pro Ser Pro Gly Ala Ala Ser Asp Asp Asp Asp Asp Val Val
 50 55 60
 Gly Ala Thr Pro Pro Ala Arg Leu Leu Glu Pro Trp Ala Gly Cys Asn
 65 70 75 80
 Gly Gly Ala Ala Ala Asp Ser Asp Ser Ser Leu Asp Glu Pro Cys Arg
 85 90 95
 Pro Gly Phe Ala Ser Glu Ser Lys Val
 100 105

<210> 7
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<212> PRT
<213> Homo sapiens

<400> 7
Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe Gln
1 5 10 15
Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn Gly
20 25 30
Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val Glu
35 40 45
Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr Glu
50 55 60
Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp Ser
65 70 75 80
Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
85 90

<210> 8
<211> 120
<212> PRT
<213> Homo sapiens

<400> 8
Asn Pro Ile Ile Tyr Ala Phe Asn Ala Asp Phe Arg Lys Ala Phe Ser
1 5 10 15
Thr Leu Leu Gly Cys Tyr Arg Leu Cys Pro Ala Thr Asn Asn Ala Ile
20 25 30
Glu Thr Val Ser Ile Asn Asn Asn Gly Ala Ala Met Phe Ser Ser His
35 40 45
His Glu Pro Arg Gly Ser Ile Ser Lys Glu Cys Asn Leu Val Tyr Leu
50 55 60
Ile Pro His Ala Val Gly Ser Ser Glu Asp Leu Lys Lys Glu Glu Ala
65 70 75 80
Ala Gly Ile Ala Arg Pro Leu Glu Lys Leu Ser Pro Ala Leu Ser Val
85 90 95
Ile Leu Asp Tyr Asp Thr Asp Val Ser Leu Glu Lys Ile Gln Pro Ile
100 105 110
Thr Gln Asn Gly Gln His Pro Thr
115 120

<210> 9
<211> 22
<212> PRT
<213> Homo sapiens

<400> 9
Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu Phe Arg Lys Ala Phe
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Leu Lys Ile Leu His Cys
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<210> 10
<211> 22
<212> PRT
<213> Homo sapiens

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<400> 10
 Asn Pro Val Ile Tyr Thr Thr Phe Asn Ile Glu Phe Arg Lys Ala Phe
 1 5 10 15
 Leu Lys Ile Leu Ser Cys
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<210> 11
 <211> 24
 <212> PRT
 <213> Homo sapiens

<400> 11
 Asn Pro Val Ile Tyr Thr Val Phe Asn Ala Glu Phe Arg Asn Val Phe
 1 5 10 15
 Arg Lys Ala Leu Arg Ala Cys Cys
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<210> 12
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 <212> PRT
 <213> Homo sapiens

<400> 12
 Asn Pro Val Ile Tyr Ala Phe Asn Ala Asp Phe Gln Lys Val Phe Ala
 1 5 10 15
 Gln Leu Leu Gly Cys Ser His Phe Cys Ser Arg Thr Pro Val Glu Thr
 20 25 30
 Val Asn Ile Ser Asn Glu Leu Ile Ser Tyr Asn Gln Asp Ile Val Phe
 35 40 45
 His Lys Glu Ile Ala Ala Ala Tyr Ile His Met Met Pro Asn Ala Val
 50 55 60
 Thr Pro Gly Asn Arg Glu Val Asp Asn Asp Glu Glu Glu Gly Pro Phe
 65 70 75 80
 Asp Arg Met Phe Gln Ile Tyr Gln Thr Ser Pro Asp Gly Asp Pro Val
 85 90 95
 Ala Glu Ser Val Trp Glu Leu Asp Cys Glu Gly Glu Ile Ser Leu Asp
 100 105 110
 Lys Ile Thr Pro Phe Thr Pro Asn Gly Phe His
 115 120

<210> 13
 <211> 47
 <212> PRT
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<400> 13
 Asn Pro Met Cys Tyr Ala Leu Cys Asn Lys Ala Phe Arg Asp Thr Phe
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 Arg Leu Leu Leu Cys Arg Trp Asp Lys Arg Arg Trp Arg Lys Ile
 20 25 30
 Pro Lys Arg Pro Gly Ser Val His Arg Thr Pro Ser Arg Gln Cys
 35 40 45

<210> 14
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 14

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Asn Pro Ala Cys Tyr Ala Leu Cys Asn Ala Thr Phe Lys Lys Thr Phe
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 Lys His Leu Leu Met Cys His Tyr Lys Asn Ile Gly Ala Thr Arg
 20 25 30

<210> 15
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 15
 Asn Pro Val Cys Tyr Ala Leu Cys Asn Lys Thr Phe Arg Thr Thr Phe
 1 5 10 15
 Lys Met Leu Leu Cys Gln Cys Asp Lys Lys Arg Arg Lys Gln
 20 25 30
 Gln Tyr Gln Gln Arg Gln Ser Val Ile Phe His Lys Arg Ala Pro Glu
 35 40 45
 Gln Ala Leu
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<210> 16
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 16
 Asn Pro Ala Cys Tyr Ala Leu Cys Asn Ala Thr Phe Lys Lys Thr Phe
 1 5 10 15
 Arg His Leu Leu Cys Gln Tyr Arg Asn Ile Gly Thr Ala Arg
 20 25 30

<210> 17
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 17
 Asn Pro Ile Cys Tyr Ala Leu Cys Asn Arg Thr Phe Arg Lys Thr Phe
 1 5 10 15
 Lys Met Leu Leu Cys Arg Trp Lys Lys Lys Val Glu Glu Lys
 20 25 30
 Leu Tyr Trp Gln Gly Asn Ser Lys Leu Pro
 35 40

<210> 18
 <211> 24
 <212> PRT
 <213> Homo sapiens

<400> 18
 Asn Pro Val Ile Tyr Ala Tyr Phe Asn Lys Asp Phe Gln Asn Ala Phe
 1 5 10 15
 Lys Lys Ile Ile Lys Cys Lys Phe
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<210> 19
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 <212> PRT

<213> Homo sapiens

<400> 19

Asn	Pro	Ile	Ile	Tyr	Thr	Met	Ser	Asn	Glu	Asp	Phe	Lys	Gln	Ala	Phe
1									10						15
His	Lys	Leu	Ile	Arg	Phe	Lys	Cys	Thr	Ser						
								25							

<210> 20

<211> 24

<212> PRT

<213> Homo sapiens

<400> 20

Asn	Pro	Leu	Leu	Tyr	Thr	Ser	Phe	Asn	Glu	Asp	Phe	Lys	Leu	Ala	Phe
1									10						15
Lys	Lys	Leu	Ile	Arg	Cys	Arg	Glu								
								20							

<210> 21

<211> 37

<212> PRT

<213> Homo sapiens

<400> 21

Asn	Pro	Ile	Ile	Tyr	Cys	Leu	Arg	Asn	Gln	Glu	Val	Lys	Arg	Ala	Leu
1									10						15
Cys	Cys	Ile	Leu	His	Leu	Tyr	Gln	His	Gln	Asp	Pro	Asp	Pro	Lys	Lys
								20	25					30	
Gly	Ser	Arg	Asn												
															35

<210> 22

<211> 27

<212> PRT

<213> Homo sapiens

<400> 22

Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn	Met	Glu	Val	Lys	Gly	Ala	Leu
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Arg	Arg	Leu	Leu	Gly	Lys	Gly	Arg	Glu	Val	Gly					
								20	25						

<210> 23

<211> 62

<212> PRT

<213> Homo sapiens

<400> 23

Asn	Pro	Leu	Phe	Tyr	Gly	Phe	Leu	Gly	Lys	Lys	Phe	Lys	Arg	Tyr	phe
1									5	10				15	
Leu	Gln	Leu	Leu	Lys	Tyr	Ile	Pro	Pro	Lys	Ala	Lys	Ser	His	Ser	Asn
									20	25			30		
Leu	Ser	Thr	Lys	Met	Ser	Thr	Leu	Ser	Tyr	Arg	Pro	Ser	Asp	Asn	Val
									35	40			45		
Ser	Ser	Ser	Thr	Lys	Pro	Ala	Pro	Cys	Phe	Glu	Val	Glu			
									55	60					

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<210> 24
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 <213> Homo sapiens

<400> 24
 Asn Pro Phe Leu Tyr Cys Phe Val Gly Asn Arg Phe Gln Gln Lys Leu
 1 5 10 15
 Arg Ser Val Phe Arg Val Pro Ile Thr Trp Leu Gln Gly Lys Arg Glu
 20 25 30
 Ser Met Ser Cys Arg Lys Ser Ser Ser Leu Arg Glu Met Glu Thr Phe
 35 40 45
 Val Ser 50

<210> 25
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 25
 Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu
 1 5 10 15
 Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro
 20 25 30
 Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser
 35 40 45
 Thr Thr Leu 50

<210> 26
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 26
 Asn Pro Leu Ile Tyr Ala Phe Ala Gly Glu Lys Phe Arg Arg Tyr Leu
 1 5 10 15
 Tyr His Leu Tyr Gly Lys Cys Leu Ala Val Leu Cys Gly Arg Ser Val
 20 25 30
 His Val Asp Phe Ser Ser Ser Glu Ser Gln Arg Ser Arg His Gly Ser
 35 40 45
 Val Leu Ser Ser Asn Phe Thr Tyr His Thr Ser Asp Gly Asp Ala Leu
 50 55 60
 Leu Leu Leu
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<210> 27
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 27
 Asn Pro Ile Leu Tyr Asn Leu Val Ser Ala Asn Phe Arg His Ile Phe
 1 5 10 15
 Leu Ala Thr Leu Ala Cys Leu Cys Pro Val Trp Arg Arg Arg Lys
 20 25 30
 Arg Pro Ala Phe Ser Arg Lys Ala Asp Ser Val Ser Asn His Thr
 35 40 45
 Leu Ser Ser Asn Ala Thr Arg Glu Thr Leu Tyr

50

55

<210> 28
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 28
 Asn Pro Ile Ile Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe
 1 5 10 15
 Lys His Ala Phe Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu
 20 25 30
 Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val
 35 40 45
 Tyr Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala
 50 55 60
 His Glu Glu Glu Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu
 65 70 75 80
 Asp Leu Thr Ser Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr
 85 90 95
 Glu Ser Phe Ser Phe Ser Ser Asn Val Leu Ser
 100 105

<210> 29
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 <212> PRT
 <213> Homo sapiens

<400> 29
 Asn Pro Trp Ile Tyr Ala Ser Phe Ser Ser Ser Val Ser Ser Glu Leu
 1 5 10 15
 Arg Ser Leu Leu Cys Cys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly
 20 25 30
 Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp
 35 40 45
 Thr Ser Ser
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<210> 30
 <211> 83
 <212> PRT
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<400> 30
 Asn Pro Val Ile Tyr Asn Leu Met Ser Gln Lys Phe Arg Ala Ala Phe
 1 5 10 15
 Arg Lys Leu Cys Asn Cys Lys Gln Lys Pro Thr Glu Lys Pro Ala Asn
 20 25 30
 Tyr Ser Val Ala Leu Asn Tyr Ser Val Ile Lys Glu Ser Asp His Phe
 35 40 45
 Ser Thr Glu Leu Asp Asp Ile Thr Val Thr Asp Thr Tyr Leu Ser Ala
 50 55 60
 Thr Lys Val Ser Phe Asp Asp Thr Cys Leu Ala Ser Glu Val Ser Phe
 65 70 75 80
 Ser Gln Ser

<210> 31
 <211> 65

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<212> PRT
 <213> Homo sapiens

<400> 31
 Asn Pro Trp Ile Tyr Met Leu Phe Thr Gly His Leu Phe His Glu Leu
 1 5 10 15
 Val Gln Arg Phe Leu Cys Cys Ser Ala Ser Tyr Leu Lys Gly Arg Arg
 20 25 30
 Leu Gly Glu Thr Ser Ala Ser Lys Lys Ser Asn Ser Ser Ser Phe Val
 35 40 45
 Leu Ser His Arg Ser Ser Ser Gln Arg Ser Cys Ser Gln Pro Ser Thr
 50 55 60
 Ala
 65

<210> 32
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 32
 Asn Pro Val Leu Tyr Ser Leu Met Ser Ser Arg Phe Arg Glu Thr Phe
 1 5 10 15
 Gln Glu Ala Leu Cys Leu Gly Ala Cys Cys His Arg Leu Arg Pro Arg
 20 25 30
 His Ser Ser His Ser Leu Ser Arg Met Thr Thr Gly Ser Thr Leu Cys
 35 40 45
 Asp Val Gly Ser Leu Gly Ser Trp Val His Pro Leu Ala Gly Asn Asp
 50 55 60
 Gly Pro Glu Ala Gln Gln Glu Thr Asp Pro Ser
 65 70 75

<210> 33
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 33
 Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala Cys
 1 5 10 15
 Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg Pro
 20 25 30
 Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser Leu
 35 40 45
 Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
 50 55 60

<210> 34
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 34
 Asn Pro Leu Val Tyr Ala Leu Ala Ser Arg His Phe Arg Ala Arg Phe
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 Arg Arg Leu Trp Pro Cys Gly Arg Arg Arg Arg His Arg Ala Arg Arg
 20 25 30
 Ala Leu Arg Arg Val Arg Pro Ala Ser Ser Gly Pro Pro Gly Cys Pro
 35 40 45
 Gly Asp Ala Arg Pro Ser Gly Arg Leu Leu Ala Gly Gly Gly Gln Gly

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50 Pro Glu Pro Arg Glu Glu Gly Pro Val His Gly Gly Glu Ala Ala Arg Gly
 55 60
 65 70 75 80
 Pro Glu

<210> 35
<211> 76
<212> PRT
<213> *Homo sapiens*

<400> 35
 Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg Arg Ala Phe
 1 5 10 15
 Ile Arg Ile Met Ser Cys Cys Lys Cys Pro Ser Gly Asp Ser Ala Gly
 20 25 30
 Lys Phe Lys Arg Pro Ile Ile Ala Gly Met Glu Phe Ser Arg Ser Lys
 35 40 45
 Ser Asp Asn Ser Ser His Pro Gln Lys Asp Glu Gly Asp Asn Pro Glu
 50 55 60
 Thr Ile Met Ser Ser Gly Asn Val Asn Ser Ser Ser
 65 70 75

<210> 36
<211> 80
<212> PRT
<213> *Homo sapiens*

<400> 36
 Asn Pro Ile Ile Tyr Ala Leu Arg Ser Lys Asp Leu Arg His Ala Phe
 1 5 10 15
 Arg Ser Met Phe Pro Ser Cys Glu Gly Thr Ala Gln Pro Leu Asp Asn
 20 25 30
 Ser Met Gly Asp Ser Asp Cys Leu His Lys His Ala Asn Asn Ala Ala
 35 40 45
 Ser Val His Arg Ala Ala Glu Ser Cys Ile Lys Ser Thr Val Lys Ile
 50 55 60
 Ala Lys Val Thr Met Ser Val Ser Thr Asp Thr Ser Ala Glu Ala Leu
 65 70 75 80

<210> 37
<211> 59
<212> PRT
<213> *Homo sapiens*

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<400> 37
Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe
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Arg Gln Leu Cys Arg Lys Pro Cys Gly Arg Pro Asp Pro Ser Ser Phe
   20          25          30
Ser Arg Pro Arg Glu Ala Thr Ala Arg Glu Arg Val Thr Ala Cys Thr
   35          40          45
Pro Ser Asp Gly Pro Gly Gly Arg Ala Ala
   50          55

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<210> 38
<211> 58
<212> PRT
<213> *Homo sapiens*

5021US_SEQ.TXT

<400> 38
Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg Asp His Ala
1 5 10 15
Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys Gln Met Gln
20 25 30
Val Ser Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser Tyr Ser
35 40 45
Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
50 55

<210> 39
<211> 66
<212> PRT
<213> Rattus norvegicus

<400> 39
Asn Gly Glu Val Gln Ala Glu Leu Arg Arg Lys Trp Arg Arg Trp His
1 5 10 15
Leu Gln Gly Val Leu Gly Trp Ser Ser Lys Ser Gln His Pro Trp Gly
20 25 30
Gly Ser Asn Gly Ala Thr Cys Ser Thr Gln Val Ser Met Leu Thr Arg
35 40 45
Val Ser Pro Ser Ala Arg Arg Ser Ser Ser Phe Gln Ala Glu Val Ser
50 55 60
Leu Val
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<210> 40
<211> 346
<212> PRT
<213> Artificial sequence

<220>
<223> hGPR3- Enhanced Receptor

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20 25 30
Pro Ala Ala Pro Leu Pro Ser Pro Lys Ala Trp Asp Val Val Leu Cys
35 40 45
Ile Ser Gly Thr Leu Val Ser Cys Glu Asn Ala Leu Val Val Ala Ile
50 55 60
Ile Val Gly Thr Pro Ala Phe Arg Ala Pro Met Phe Leu Leu Val Gly
65 70 75 80
Ser Leu Ala Val Ala Asp Leu Leu Ala Gly Leu Gly Leu Val Leu His
85 90 95
Phe Ala Ala Val Phe Cys Ile Gly Ser Ala Glu Met Ser Leu Val Leu
100 105 110
Val Gly Val Leu Ala Met Ala Phe Thr Ala Ser Ile Gly Ser Leu Leu
115 120 125
Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Asn Ala Leu Thr Tyr
130 135 140
Tyr Ser Glu Thr Thr Val Thr Arg Thr Tyr Val Met Leu Ala Leu Val
145 150 155 160
Trp Gly Gly Ala Leu Gly Leu Gly Leu Pro Val Leu Ala Trp Asn
165 170 175
Cys Leu Asp Gly Leu Thr Thr Cys Gly Val Val Tyr Pro Leu Ser Lys
180 185 190

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Asn His Leu Val Val Leu Ala Ile Ala Phe Phe Met Val Phe Gly Ile
 195 200 205
 Met Leu Gln Leu Tyr Ala Gln Ile Cys Arg Ile Val Cys Arg His Ala
 210 215 220
 Gln Gln Ile Ala Leu Gln Arg His Leu Leu Pro Ala Ser His Tyr Val
 225 230 235 240
 Ala Thr Arg Lys Gly Ile Ala Thr Leu Ala Val Val Leu Gly Ala Phe
 245 250 255
 Ala Ala Cys Trp Leu Pro Phe Thr Val Tyr Cys Leu Leu Gly Asp Ala
 260 265 270
 His Ser Pro Pro Leu Tyr Thr Tyr Leu Thr Leu Leu Pro Ala Thr Tyr
 275 280 285
 Asn Ser Met Ile Asn Pro Ile Ile Tyr Ala Phe Arg Asn Gln Asp Val
 290 295 300
 Gln Lys Val Leu Trp Ala Val Cys Cys Cys Ala Ala Ala Arg Gly
 305 310 315 320
 Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala
 325 330 335
 Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
 340 345

<210> 41

<211> 1041

<212> DNA

<213> Artificial sequence

<220>

<223> hGPR3- Enhanced Receptor

<400> 41

atggatgtgg gtcgaggcag ccctctggcc tggctctcag ctggctcagg caacgtgaat 60
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 aaggccctggg atgttgtgtct ctgcatttcga ggcacccctgg tgfcctgcga gaatgcgcta 180
 gtggatgtgg tcatcgtggg cactctgtcc ttccctggcc ccatgtttccct gctgggtggc 240
 agccctggcc tggcagacact gctggcaggc ctggggctgg tcctgcaccc ttgtgcgtgc 300
 ttctgcatcg gctcagccggat gatggagccgt tggtgtgggg gcgtgcgtgc aatggccctt 360
 actgcgcacca tcggcagtc actggccatc actgtgcaccc gtcacccctt tctgtacaat 420
 gccttcacactt acttgcacca gacaacatcg acacggaccc ttgtgtatgc ggcctttagt 480
 tggggagggtg cccctggccctt ggggtctgtg cctgtgtggg ccgtggaaatcg cctggatggc 540
 ctgaccacat gtgcgtgtgtt ttatccatc tccaaagaacc atctggatgt tctggccatt 600
 gccttcctca tgggtttttggg catatcgatcg cagcttcacg cccaaatctcg ccgcattcg 660
 tgcgcgcattatggcc cccaggatcgatcg cactatcgcc tggtgtgtgg gaccccttgc gcgcgtgtgg 720
 gccaccccgca aggccatcgatcg cactatcgcc tggtgtgtgg gaccccttgc gcgcgtgtgg 780
 ttgccttcatac cttgttactgtggt gatggccacactt cttccacccatctt ctacacccat 840
 cttacacctgc tccctggccac ctacaactcc atgtcaaccc ctatcatcta cgccttcgg 900
 aacccaggatcg tgcgaaatcg gctgtgggtc gtcgtgtgtc gctgtgcggc cgcacgggg 960
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 gccaaggacaca cttcatcgatcg a 1041

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<211> 378

<212> PRT

<213> Artificial sequence

<220>

<223> hGPR6- Enhanced Receptor

<400> 42

Met Asn Ala Ser Ala Ala Ser Leu Asn Asp Ser Gln Val Val Val
 1 5 10 15
 Ala Ala Glu Gly Ala Ala Ala Ala Ala Thr Ala Ala Gly Gly Pro Asp
 20 25 30

5021US_SEQ.TXT

Thr Gly Glu Trp Gly Pro Pro Ala Ala Ala Ala Leu Gly Ala Gly Gly
 35 40 45
 Gly Ala Asn Gly Ser Leu Glu Leu Ser Ser Gln Leu Ser Ala Gly Pro
 50 55 60
 Pro Gly Leu Leu Leu Pro Ala Val Asn Pro Trp Asp Val Leu Leu Cys
 65 70 75 80
 Val Ser Gly Thr Val Ile Ala Gly Glu Asn Ala Leu Val Val Ala Leu
 85 90 95
 Ile Ala Ser Thr Pro Ala Leu Arg Thr Pro Met Phe Val Leu Val Gly
 100 105 110
 Ser Leu Ala Thr Ala Asp Leu Leu Ala Gly Cys Gly Leu Ile Leu His
 115 120 125
 Phe Val Phe Gln Tyr Leu Val Pro Ser Glu Thr Val Ser Leu Leu Thr
 130 135 140
 Val Gly Phe Leu Val Ala Ser Phe Ala Ala Ser Val Ser Ser Leu Leu
 145 150 155 160
 Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Asn Ala Leu Thr Tyr
 165 170 175
 Tyr Ser Arg Arg Thr Leu Leu Gly Val His Leu Leu Leu Ala Ala Thr
 180 185 190
 Trp Thr Val Ser Leu Gly Leu Gly Leu Leu Pro Val Leu Gly Trp Asn
 195 200 205
 Cys Leu Ala Glu Arg Ala Ala Cys Ser Val Val Arg Pro Leu Ala Arg
 210 215 220
 Ser His Val Ala Leu Leu Ser Ala Ala Phe Phe Met Val Phe Gly Ile
 225 230 235 240
 Met Leu His Leu Tyr Val Arg Ile Cys Gln Val Val Trp Arg His Ala
 245 250 255
 His Gln Ile Ala Leu Gln Gln His Cys Leu Ala Pro Pro His Leu Ala
 260 265 270
 Ala Thr Arg Lys Gly Val Gly Thr Leu Ala Val Val Leu Gly Thr Phe
 275 280 285
 Gly Ala Ser Trp Leu Pro Phe Ala Ile Tyr Cys Val Val Gly Ser His
 290 295 300
 Glu Asp Pro Ala Val Tyr Thr Tyr Ala Thr Leu Pro Ala Thr Tyr
 305 310 315 320
 Asn Ser Met Ile Asn Pro Ile Ile Tyr Ala Phe Arg Asn Gln Glu Ile
 325 330 335
 Gln Arg Ala Leu Trp Leu Leu Cys Gly Cys Ala Ala Ala Arg Gly
 340 345 350
 Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala
 355 360 365
 Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
 370 375

<210> 43

<211> 1137

<212> DNA

<213> Artificial Sequence

<220>

<223> hGPR6- Enhanced Receptor

<400> 43

atgaacgcga gcgcgcgcctc gctcaacgcat tcccagggtgg tggtagtggc ggccgaaggaa 60
 gcggcgccgg cggccacagc agcagggggg ccggacacgg gcaatgggg accccctgct 120
 gcggcgctc tagggacccgg cggccggact aatgggtctc tggagctgc ctccgacgtc 180
 tcggctggggc caccgggact cctctggccaa gcggtgaatc cgtggggacgt gctctgtgc 240
 gtgtcggggat cagtgatcgc tggggaaaac ggcgtgtgg tggcgctcat cgcgtccact 300
 ccggcgctgc gcacgcctt gttcgtgtcgtg gtggcggactc tggccaccgc tgacactgtt 360
 gcggcgctgtg gccctatctt gcacccgtgt tttccagtaact tggtgccctc ggagactgtg 420
 agtctgtctca cggtgggctt cctcggtggcc tccttcggcc cctctgtcag cagcgtctg 480

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 gccattacgg tggaccgcta cctgtccctg tataacgcgc tcacccattata ctcgcgcggg 540
 accctgtgg gctgtcacct cctgttgcg gccacttggg cctgtccctt aggccgtggg 600
 ctgtgtccgg tgcgtggctg gaactgcgg gcaagggcgg ccgcgtcgag cgtgggtgcg 660
 ccgcgtggcgc gcaaggcactg ggcttcgtt cccgcgcct tcttcatgtt ctgcgcgc 720
 atgtgcaccc tgcgtggctg cacttcggcgt gtggctggcgt gccaaggcgc ccaatgcgc 780
 ctgcaggcgcg actggcgtggc gccacccat ctcgtgcgc ccaagaaaggg tgggtgtaca 840
 ctggctgtgg tgcgtggcac ttccggccg aacggcgtgc ccttcgcctt ctatgcgtg 900
 gtggcgcggc atgaggaccc ggccgtctac acttaacggc ccctgtgcgc cgccacccatc 960
 aacttcatgaa tcaatccat cactatggc ttccggcaacc agagatcga ggcgcgcgg 1020
 tggctcttcg tctgtggctg tgccggccgcg cggggacgcg ccccaacccag ctgggtccc 1080
 caagatgatg cctgcaccac cgccaggctcc tccctggcga aggacacttc atcgtga 1137

<210> 44

<211> 350

<212> PRT

<213> Artificial Sequence

<220>

<223> hGPR12- Enhanced Receptor

<400> 44

Met Asn Glu Asp Leu Lys Val Asn Leu Ser Gly Leu Pro Arg Asp Tyr
 1 5 10 15
 Leu Asp Ala Ala Ala Ala Glu Asn Ile Ser Ala Ala Val Ser Ser Arg
 20 25 30
 Val Pro Ala Val Glu Pro Glu Pro Glu Leu Val Val Asn Pro Trp Asp
 35 40 45
 Ile Val Leu Cys Thr Ser Gly Thr Leu Ile Ser Cys Glu Asn Ala Ile
 50 55 60
 Val Val Leu Ile Ile Phe His Asn Pro Ser Leu Arg Ala Pro Met Phe
 65 70 75 80
 Leu Leu Ile Gly Ser Leu Ala Leu Ala Asp Leu Leu Ala Gly Ile Gly
 85 90 95
 Leu Ile Thr Asn Phe Val Phe Ala Tyr Leu Leu Gln Ser Glu Ala Thr
 100 105 110
 Lys Leu Val Thr Ile Gly Leu Ile Val Ala Ser Phe Ser Ala Ser Val
 115 120 125
 Cys Ser Leu Leu Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Tyr
 130 135 140
 Ala Leu Thr Tyr His Ser Gln Arg Thr Val Thr Phe Thr Tyr Val Met
 145 150 155 160
 Leu Val Met Leu Trp Gly Thr Ser Ile Cys Leu Gly Leu Leu Pro Val
 165 170 175
 Met Gly Trp Asn Cys Leu Arg Asp Glu Ser Thr Cys Ser Val Val Arg
 180 185 190
 Pro Leu Thr Lys Asn Asn Ala Ala Ile Leu Ser Val Ser Phe Leu Phe
 195 200 205
 Met Phe Ala Leu Met Leu Gln Leu Tyr Ile Gln Ile Cys Lys Ile Val
 210 215 220
 Met Arg His Ala His Gln Ile Ala Leu Gln His His Phe Leu Ala Thr
 225 230 235 240
 Ser His Tyr Val Thr Thr Arg Lys Gly Val Ser Thr Leu Ala Ile Ile
 245 250 255
 Leu Gly Thr Phe Ala Ala Cys Trp Met Pro Phe Thr Leu Tyr Ser Leu
 260 265 270
 Ile Ala Asp Tyr Thr Tyr Pro Ser Ile Tyr Thr Tyr Ala Thr Leu Leu
 275 280 285
 Pro Ala Thr Tyr Asn Ser Ile Ile Asn Pro Val Ile Tyr Ala Phe Arg
 290 295 300
 Asn Gln Gln Ile Gln Lys Ala Leu Cys Leu Ile Cys Cys Gly Cys Ala
 305 310 315 320
 Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser
 325 330 335

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Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
340 345 350

<210> 45
<211> 1053
<212> DNA
<213> Artificial Sequence

<220>
<223> hGPR12- Enhanced Receptor

<400> 45
atgaatgaag acctgaaggt caatttaaagc gggctgcctc gggattattt agatgccgt 60
gctccggaga acatctggc tgctgttcc tccgggttc ctgcgttgc gccagagcct 120
gagctcgtag tcaacccttc ggacatgtc ttgttaccc cggaaacccc cattctgt 180
gaaaatgcctt ttgtgttc tatcatcttc cacaacccc gcttcgagc acccatgttc 240
ctgctatag gcagcttgcg tcttcgacag ctgtggccg gcatggact cattcaaat 300
tttgttttg cttacactgtc tcagtcgac gccaccaagc tggtcacgtat cggccctatt 360
gtgccttcgat tctgtccgt tgatgttcgat ttgtgttgc tcaactgttg ccgttacttc 420
tcaactgtact acgtcttcgtat gtacccatcg gagaggacgg tcacgtttat ctatgtatcg 480
ctgcgttcgcg tctgggggac ctccatctgc ctgtgggttc tgccgttcat gggctggaaat 540
tgcccccggag acgagtccac ttcgcgtgc gtcagacccg tcaccaagaa caacgcggcc 600
atcccttcgg tgccttcctt ctatgtttt gcgttcatgc ttcaagcttca catccagatc 660
tgatagatgt tgatgtggccg cgcggccatcg atagcccttc agcaccactt cctggccacg 720
tcgcatactg tgacccatccg gaaagggttc tccaccccttgc ctatccatcc ggggacgttt 780
gctcttgcgt ggatgccttat cacccttat tcctgtatag cggattacac ctacccttcc 840
atccataacctt acggccacctt cttgcggccg acctacaaat ccatcatcaa ccttgcata 900
tatgtttca gaaaccaaga gatccagaaa gcgcgttgc tcatttgcgt cggctgcgcg 960
gcccacggg gacgcaccccc acccagccgtt ggtccccaaat gatgatccgtt caccacccgc 1020
agttccctcc tggccaaagga cacttcatcg tga 1053

<210> 46
<211> 388
<212> PRT
<213> Artificial Sequence

<220>
<223> hsREB3- Enhanced Receptor

<400> 46
Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
1 5 10 15
Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
20 25 30
Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
35 40 45
Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
50 55 60
Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
65 70 75 80
Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
85 90 95
Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
100 105 110
Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
115 120 125
Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
130 135 140
Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
145 150 155 160
Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
165 170 175

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Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
 180 185 190
 Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu
 195 200 205
 Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro
 210 215 220
 Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln
 225 230 235 240
 Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro
 245 250 255
 Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu
 260 265 270
 Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe
 275 280 285
 Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val
 290 295 300
 Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg
 305 310 315 320
 Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn
 325 330 335
 Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Arg
 340 345 350
 Thr His Ala Pro Cys Ala Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu
 355 360 365
 Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys
 370 375 380
 Asp Thr Ser Ser
 385

<210> 47

<211> 1167

<212> DNA

<213> Artificial Sequence

<220>

<223> hsREB3- Enhanced Receptor

<400> 47

atggccaaaca ctaccggaga gcctgaggag gtgagccgcg ctctgtcccc accgtccgc 60
 tcagcttatg tgaagctggt actgtctggg ctgattatgt gcgtgagcc ggcgggtaaac 120
 gccatcttgc cccctgggt gctcaaggag ctgcgtccgc acaaggctcc ttactacttc 180
 ctgtctggacc tggctctggc ctggatggata cgccttcgcg ctgtctggcc ctttgtctg 240
 gctctgtggc gccacggctt ttcatggacc ttcaatgcgac tcacgtcaca gatttgtggc 300
 ttatggccg tgccttttgc ctccatgcg cgccttcgcg tgcgttcgcat cagcgatcacc 360
 cgcatacattgg ccatacgccca ccacccgccttc tacggcaagg gcatgacact ctggacatgc 420
 gcggtcgta ttcgtatggc ctggacccctg ttcgtggcca tggcccttcc acctgtcttt 480
 gacgtggcc ctatcaaggat tattccggag gaggacaggat gcacattttgc gcacatcgat 540
 ttcaaggccca atgacacgctt gggtttccat cttatgtggc ctgtgttcat ggcagctacc 600
 catgtgtctt acggcaaggctt gcgtcccttc gagatgttcgcg accgcgaat gaaaggcttgc 660
 catgtgtgc cagccatcgcc ccagaacttgc acatccatgcg tgcctccggc caccggccag 720
 gctgtcgcca actggatgcg cggctttggc cttgtggccca tgccaccaac cctgtctgggt 780
 atccggcaga atgggcatgc agccacggccg cggctacttgc gcatggacgaa ggtcagggtt 840
 gaaaaggcage tggggccgcg attcacactgc tcttttgcgtt cctctgttca 900
 cccatcatcg tggctctgcata ctggccatgtt ttttgtaaag cctgtgtgtt gccccaccgc 960
 tacctggccca ctgtcttttg gatggacttgc gcccaggctg cccgtcaaccc aatttgtctgc 1020
 ttctctgtca acaaggactt caaaggatgc ctggggactc acggcccttc cgcggccgc 1080
 cggggacgcg ccccaaccat cttgggttccca caagatgatgtt cttgtcaccac cggccaggctcc 1140
 tccctggccca aggacacttc atcgtga 1167

<210> 48

<211> 388

<212> PRT

<213> Artificial Sequence

<220>

<223> hSREB2- Enhanced Receptor

<400> 48

Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
 1 5 10 15
 Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
 20 25 30
 Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35 40 45
 Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50 55 60
 Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65 70 75 80
 Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85 90 95
 Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
 100 105 110
 Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
 115 120 125
 Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
 130 135 140
 Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
 145 150 155 160
 Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His
 165 170 175
 Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala
 180 185 190
 Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe
 195 200 205
 Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
 210 215 220
 Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
 225 230 235 240
 Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu
 245 250 255
 Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
 260 265 270
 Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
 275 280 285
 Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
 290 295 300
 Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
 305 310 315 320
 Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
 325 330 335
 Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr
 340 345 350
 Thr Leu Leu Tyr Cys Ala Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu
 355 360 365
 Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys
 370 375 380
 Asp Thr Ser Ser
 385

<210> 49

<211> 1167

<212> DNA

<213> Artificial Sequence

<220>

<223> hsREB2- Enhanced Receptor

<400> 49

atggcgaact	atagccatgc	actgtgacaac	attttgc当地	atctctcgcc	tctaaacagcc	60
ttttcgaaac	tgacttc当地	gggtttcata	ataggaggc	gcgttgttgg	caacctctg	120
atcttc当地	tgtctgtgaa	agataaagacc	ttgc当地	actgttgg	cccttacta	180
gatctt当地	gttc当地	gttccatgtt	gttccatgtt	cccttactt	ttccctgtt	240
gtcaaaaatg	gctt当地	gactt当地	actctgactt	gcaactgtat	tgcccttctg	300
ggggttt当地	ccctgtt当地	caactgtt当地	atgtt当地	gcatc当地	caccagata	360
tttagt当地	ccatcatc	ccatcatc	aaaggagg	cctttggat	gtgtctgct	420
gtgtatc当地	tgtgtggat	tgtgtggat	gcatggat	ttcccccggt	tttagacgt	480
ggcactt当地	cattt当地	ggaggaaat	caatgc当地	tccaaacacc	ctccctcagg	540
gctaata当地	cctt当地	ttatgtc当地	tttgc当地	ttccctctag	cacacagctt	600
gttctt当地	actgtt当地	tttgc当地	gttcc当地	aaatgtt当地	agtc当地	660
gttcc当地	tc当地	tc当地	tc当地	tc当地	tc当地	720
gcaat当地	tc当地	tc当地	tc当地	tc当地	tc当地	780
caaaat当地	acacc	acacc	acacc	ccaccc	ccaccc	840
aaaagaatca	gc当地	gc当地	gc当地	gc当地	gc当地	900
tactt当地	ggctt当地	ttt当地	ttt当地	ttt当地	ttt当地	960
ctt当地	ttt当地	ttt当地	ttt当地	ttt当地	ttt当地	1020
ttt当地	ttt当地	ttt当地	ttt当地	ttt当地	ttt当地	1080
ccccggacca	cccc	cccc	cccc	cccc	cccc	1140
tccctggcca	aggacactt	aggacactt	aggacactt	aggacactt	aggacactt	1167

<210> 50

<211> 364

<212> PRT

<213> Artificial sequence

<220>

<223> hgPR8- Enhanced Receptor

<400> 50

Met Gln	Ala	Ala	Gly	His	Pro	Glu	Pro	Leu	Asp	Ser	Arg	Gly	Ser	Phe	
1	5	5	10	10	10	10	10	10	10	10	10	15	15	15	
Ser	Leu	Pro	Thr	Met	Gly	Ala	Asn	Val	Ser	Gln	Asp	Asn	Gly	Thr	Gly
20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20
His	Asn	Ala	Thr	Phe	Ser	Glu	Pro	Leu	Pro	Phe	Leu	Tyr	Val	Leu	Leu
35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35
Pro	Ala	Val	Tyr	Ser	Gly	Ile	Cys	Ala	Val	Gly	Leu	Thr	Gly	Asn	Thr
50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50
Ala	Val	Ile	Leu	Val	Ile	Leu	Arg	Ala	Pro	Lys	Met	Lys	Thr	Val	Thr
65	65	65	65	65	65	65	65	65	65	65	65	65	65	65	65
Asn	Val	Phe	Ile	Leu	Asn	Leu	Ala	Val	Ala	Asp	Gly	Leu	Phe	Thr	Leu
85	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85
Val	Leu	Pro	Val	Asn	Ile	Ala	Glu	His	Leu	Leu	Gln	Tyr	Trp	Pro	Phe
100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
Gly	Glu	Leu	Leu	Cys	Lys	Leu	Val	Leu	Ala	val	Asp	His	Tyr	Asn	Ile
115	115	115	115	115	115	115	115	115	115	115	115	115	115	115	115
Phe	Ser	Ser	Ile	Tyr	Phe	Leu	Ala	Val	Met	Ser	Val	Asp	Arg	Tyr	Leu
130	130	130	130	130	130	130	130	130	130	130	130	130	130	130	130
Val	Val	Leu	Ala	Thr	Val	Arg	Ser	Arg	His	Met	Pro	Trp	Arg	Thr	Tyr
145	145	145	145	145	145	145	145	145	145	145	145	145	145	145	145
Arg	Gly	Ala	Lys	Val	Ala	Ser	Leu	Cys	Val	Trp	Leu	Gly	Val	Thr	Val
165	165	165	165	165	165	165	165	165	165	165	165	165	165	165	165
Leu	Val	Leu	Pro	Phe	Phe	Ser	Phe	Ala	Gly	Val	Tyr	Ser	Asn	Glu	Leu
180	180	180	180	180	180	180	180	180	180	180	180	180	180	180	180
Gln	Val	Pro	Ser	Cys	Gly	Leu	Ser	Phe	Pro	Trp	Pro	Glu	Arg	Val	Trp
195	195	195	195	195	195	195	195	195	195	195	195	195	195	195	195
Phe	Lys	Ala	Ser	Arg	Val	Tyr	Thr	Leu	Val	Leu	Gly	Phe	Val	Leu	Pro
210	210	210	210	210	210	210	210	210	210	210	210	210	210	210	210
Val	Cys	Thr	Ile	Cys	Val	Leu	Tyr	Thr	Asp	Leu	Leu	Arg	Arg	Leu	Arg

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225	230	235	240
Ala Val Arg Leu Arg Ser Gly Ala Lys Ala Leu Gly Lys Ala Arg Arg			
245	250	255	
Lys Val Thr Val Leu Val Val Leu Ala Val Cys Leu Leu Cys			
260	265	270	
Trp Thr Pro Phe His Leu Ala Ser Val Val Ala Leu Thr Thr Asp Leu			
275	280	285	
Pro Gln Thr Pro Leu Val Ile Ser Met Ser Tyr Val Ile Thr Ser Leu			
290	295	300	
Ser Tyr Ala Asn Ser Cys Leu Asn Pro Phe Leu Tyr Ala Phe Leu Asp			
305	310	315	320
Asp Asn Phe Arg Lys Asn Phe Arg Ser Ile Leu Arg Cys Ala Ala Ala			
325	330	335	
Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr			
340	345	350	
Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser			
355	360		

<210> 51

<211> 1095

<212> DNA

<213> Artificial sequence

<220>

<223> hGPR8- Enhanced Receptor

<400> 51

atcgaggccg	ctggggcaccc	agagccccctt	gacagcaggg	gctcccttctc	ccctccccacg	60
atgggtgcaca	acgttcttc	ggacaatggc	actggccaca	atggccaccc	ctccgagcc	120
ctggccgttc	tctatgtct	cctggccccc	gtgtacttcg	ggatctgtc	tgtggggctg	180
actgtggcaacc	cggggcgtcat	ccttgtaattc	ctaaggggcgc	ccaaatgtgaa	gacgggtacc	240
aaatgttca	tccgtggaccc	ggccgtccgc	gacggggctct	tcaatgtgtt	actggccgtc	300
aaatcgcgg	agcaggctgt	gcaatgtactgg	cccttcgggg	agctgtctcg	caagctgtgg	360
ctggccgtcg	accatctacaa	catcttctcc	agcatctact	tccatggcgt	gatgagcgt	420
gaccgtatcc	tgggtgtct	ggccaccgtg	aggttccccc	acatggccctg	gcgcacccat	480
cggggatcc	agggtggccag	cctgtgttgc	tggctggggc	tcaatgttct	ggttttgc	540
tttttcttctt	tcgtggcgt	ctacagcaac	gagctgcagg	tcccaagctg	tgggttgcage	600
tttcgttggc	ccgagcgggt	ctgttcaag	ggccaggctg	tctacacttt	ggctctgggg	660
tttcgtgttc	ccgttgtcac	catctgtgt	cttcaacacag	acccttcgtc	cagggtcg	720
gcccgtggc	tccgtctgg	agccaaaggct	ctaggcaagg	ccaggcggaa	ggtgaccgtc	780
ctgtgtcttc	tcgtgtccgc	cgtgtccca	ctctgtggaa	cgcccttc	ctctggctct	840
gtctgtggcc	tgaccacggc	cctggccccc	accccttgc	tcatcgtat	gtcttacgtc	900
atccacccat	tcgtactcgt	caatctgtc	ctgttacccct	tcccttacgt	cttttttagat	960
gacaatcc	ggaaagaccc	ccgcgcata	ttggggctgc	cgccggcacc	ggggacgcacc	1020
ccacccatcc	tgggtcccca	agatgagtcc	tgccaccccg	ccagtcctc	cctggccaag	1080
gacacccat	ctgtgtgt					1095

<210> 52

<211> 419

<212> PRT

<213> Artificial sequence

<220>

<223> hGPR22-Enhanced Receptor

<400> 52

Met Cys Phe Ser Pro Ile Leu Glu Ile Asn Met Gln Ser Glu Ser Asn			
1	5	10	15
Ile Thr Val Arg Asp Asp Ile Asp Asp Ile Asn Thr Asn Met Tyr Gln			
20	25	30	
Pro Leu Ser Tyr Pro Leu Ser Phe Gln Val Ser Leu Thr Gly Phe Leu			
35	40	45	

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Met Leu Glu Ile Val Leu Gly Leu Gly Ser Asn Leu Thr Val Leu Val
 50 55 60
 Leu Tyr Cys Met Lys Ser Asn Leu Ile Asn Ser Val Ser Asn Ile Ile
 65 70 75 80
 Thr Met Asn Leu His Val Leu Asp Val Ile Ile Cys Val Gly Cys Ile
 85 90 95
 Pro Leu Thr Ile Val Ile Leu Leu Leu Ser Leu Glu Ser Asn Thr Ala
 100 105 110
 Leu Ile Cys Cys Phe His Glu Ala Cys Val Ser Phe Ala Ser Val Ser
 115 120 125
 Thr Ala Ile Asn Val Phe Ala Ile Thr Leu Asp Arg Tyr Asp Ile Ser
 130 135 140
 Val Lys Pro Ala Asn Arg Ile Leu Thr Met Gly Arg Ala Val Met Leu
 145 150 155 160
 Met Ile Ser Ile Trp Ile Phe Ser Phe Phe Ser Phe Leu Ile Pro Phe
 165 170 175
 Ile Glu Val Asn Phe Phe Ser Leu Gln Ser Gly Asn Thr Trp Glu Asn
 180 185 190
 Lys Thr Leu Leu Cys Val Ser Thr Asn Glu Tyr Tyr Thr Glu Leu Gly
 195 200 205
 Met Tyr Tyr His Leu Leu Val Gln Ile Pro Ile Phe Phe Phe Thr Val
 210 215 220
 Val Val Met Leu Ile Thr Tyr Thr Lys Ile Leu Gln Ala Leu Asn Ile
 225 230 235 240
 Arg Ile Gly Thr Arg Phe Ser Thr Gly Gln Lys Lys Lys Ala Arg Lys
 245 250 255
 Lys Lys Thr Ile Ser Leu Thr Thr Gln His Glu Ala Thr Asp Met Ser
 260 265 270
 Gln Ser Ser Gly Gly Arg Asn Val Val Phe Gly Val Arg Thr Ser Val
 275 280 285
 Ser Val Ile Ile Ala Leu Arg Arg Ala Val Lys Arg His Arg Glu Arg
 290 295 300
 Arg Glu Arg Gln Lys Arg Val Phe Arg Met Ser Leu Leu Ile Ile Ser
 305 310 315 320
 Thr Phe Leu Leu Cys Trp Thr Pro Ile Ser Val Leu Asn Thr Thr Ile
 325 330 335
 Leu Cys Leu Gly Pro Ser Asp Leu Leu Val Lys Leu Arg Leu Cys Phe
 340 345 350
 Leu Val Met Ala Tyr Gly Thr Thr Ile Phe His Pro Leu Leu Tyr Ala
 355 360 365
 Phe Thr Arg Gln Lys Phe Gln Lys Val Leu Lys Ser Lys Met Lys Lys
 370 375 380
 Arg Val Val Cys Ala Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly
 385 390 395 400
 Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp
 405 410 415
 Thr Ser Ser

<210> 53

<211> 1260

<212> DNA

<213> Artificial Sequence

<220>

<223> hGPR22-Enhanced Receptor

<400> 53

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caatgtttt tcacccgatt tttttttttt gaaatgtgttggggacttgg cggccatcc 180
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atatgtatcca	ttttggattt	ttcttttttc	ttttttctgt	ttttttttat	ttggggtaata	540
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acattttttc	tctgttggac	accattttt	ttttttataa	ccacccattt	atgttttaggc	1020
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atattttttcc	ttcttataata	ttgttttttt	tttttttttt	tttttttttt	tttggaaaatgt	1140
aaatgtttttt	aaatgtttttt	tttttttttt	tttttttttt	tttttttttt	caggccgggt	1200
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<210> 54

<211> 370

<212> PRT

<213> Artificial Sequence

<220>

<223> beta2AR-v2R chimera

<400> 54

1 Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
 5 10 15
 Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
 20 25 30
 35 40 45
 Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
 50 55 60
 Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
 65 70 75 80
 Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
 85 90 95
 Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
 100 105 110
 Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
 115 120 125
 Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
 130 135 140
 Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
 145 150 155 160
 Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
 165 170 175
 Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
 180 185 190
 Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
 195 200 205
 Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln
 210 215 220
 Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
 225 230 235 240
 His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His
 245 250 255
 Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu
 260 265 270
 Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro

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275	280	285		
Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg	290	295	300	
Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly	305	310	315	320
Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe	325	330	335	
Gln Glu Leu Leu Cys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro	340	345	350	
Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr	355	360	365	
Ser Ser	370			

<210> 55
<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> MOR-V2R chimera

<400> 55

Met Asp Ser Ser Thr Gly Pro Gly Asn Thr Ser Asp Cys Ser Asp Pro	1	5	10	15
Leu Ala Gln Ala Ser Cys Ser Pro Ala Pro Gly Ser Trp Leu Asn Leu	20	25	30	
Ser His Val Asp Gly Asn Gln Ser Asp Pro Cys Gly Leu Asn Arg Thr	35	40	45	
Gly Leu Gly Gly Asn Asp Ser Leu Cys Pro Gln Thr Gly Ser Pro Ser	50	55	60	
Met Val Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val Cys Val	65	70	75	80
Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val Arg Tyr	85	90	95	
Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu	100	105	110	
Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Asn Tyr	115	120	125	
Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile Val Ile	130	135	140	
Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Cys Thr	145	150	155	160
Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu	165	170	175	
Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Val Asn Val Cys Asn Trp	180	185	190	
Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala Thr Thr	195	200	205	
Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Pro	210	215	220	
Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile Phe Ala	225	230	235	240
Phe Ile Met Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Ile	245	250	255	
Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp	260	265	270	
Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Ala Val	275	280	285	
Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala	290	295	300	
Leu Ile Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe				

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305	310	315	320
Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys	Leu Asn Pro Val Leu	Tyr	
325	330	335	
Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys	Phe Arg Glu Phe Cys	Ala	
340	345	350	
Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu	Gly Pro Gln Asp Glu	Ser	
355	360	365	
Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys	Asp Thr Ser Ser		
370	375	380	

<210> 56
<211> 382
<212> PRT
<213> Artificial sequence

<220>
<223> D1AR-V2R chimera

<400> 56
Met Ala Pro Asn Thr Ser Thr Met Asp Glu Ala Gly Leu Pro Ala Glu
1 5 10 15
Arg Asp Phe Ser Phe Arg Ile Leu Thr Ala Cys Phe Leu Ser Leu Leu
20 25 30
Ile Leu Ser Thr Leu Leu Gly Asn Thr Leu Val Cys Ala Ala Val Ile
35 40 45
Arg Phe Arg His Leu Arg Ser Lys Val Thr Asn Phe Phe Val Ile Ser
50 55 60
Leu Ala Val Ser Asp Leu Leu Val Ala Val Leu Val Met Pro Trp Lys
65 70 75 80
Ala Val Ala Glu Ile Ala Gly Phe Trp Pro Phe Gly Ser Phe Cys Asn
85 90 95
Ile Trp Val Ala Phe Asp Ile Met Cys Ser Thr Ala Ser Ile Leu Asn
100 105 110
Leu Cys Val Ile Ser Val Asp Arg Tyr Trp Ala Ile Ser Ser Pro Phe
115 120 125
Gln Tyr Glu Arg Lys Met Thr Pro Lys Ala Ala Phe Ile Leu Ile Ser
130 135 140
Val Ala Trp Thr Leu Ser Val Leu Ile Ser Phe Ile Pro Val Gln Leu
145 150 155 160
Ser Trp His Lys Ala Lys Pro Thr Trp Pro Leu Asp Gly Asn Phe Thr
165 170 175
Ser Leu Glu Asp Thr Glu Asp Asp Asn Cys Asp Thr Arg Leu Ser Arg
180 185 190
Thr Tyr Ala Ile Ser Ser Ser Leu Ile Ser Phe Tyr Ile Pro Val Ala
195 200 205
Ile Met Ile Val Thr Tyr Thr Ser Ile Tyr Arg Ile Ala Gln Lys Gln
210 215 220
Ile Arg Arg Ile Ser Ala Leu Glu Arg Ala Ala Val His Ala Lys Asn
225 230 235 240
Cys Gln Thr Thr Ala Gly Asn Gly Asn Pro Val Glu Cys Ala Gln Ser
245 250 255
Glu Ser Ser Phe Lys Met Ser Phe Lys Arg Glu Thr Lys Val Leu Lys
260 265 270
Thr Leu Ser Val Ile Met Gly Val Phe Val Cys Cys Trp Leu Pro Phe
275 280 285
Phe Ile Ser Asn Cys Met Val Pro Phe Cys Gly Ser Glu Glu Thr Gln
290 295 300
Pro Phe Cys Ile Asp Ser Ile Thr Phe Asp Val Phe Val Trp Phe Gly
305 310 315 320
Trp Ala Asn Ser Ser Leu Asn Pro Ile Ile Tyr Ala Phe Asn Ala Asp
325 330 335
Phe Gln Lys Ala Phe Ser Thr Leu Leu Gly Cys Tyr Arg Leu Cys Ala

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340	345	350
Ala Ala Arg Gly Arg Thr Pro Pro Ser	Leu Gly Pro Gln Asp Glu Ser	
355	360	365
Cys Thr Thr Ala Ser Ser Ser	Leu Ala Lys Asp Thr Ser Ser	
370	375	380

<210> 57
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> 5HT1AR-V2R chimera

<400> 57
Met Asp Val Leu Ser Pro Gly Gln Gly Asn Asn Thr Thr Ser Pro Pro
1 5 10 15
Ala Pro Phe Glu Thr Gly Gly Asn Thr Thr Gly Ile Ser Asp Val Thr
20 25 30
val Ser Tyr Gln Val Ile Thr Ser Leu Leu Leu Gly Thr Leu Ile Phe
35 40 45
cys Ala Val Leu Gly Asn Ala Cys Val Val Ala Ala Ile Ala Leu Glu
50 55 60
Arg Ser Leu Gln Asn Val Ala Asn Tyr Leu Ile Gly Ser Leu Ala Val
65 70 75 80
Thr Asp Leu Met Val Ser Val Leu Val Leu Pro Met Ala Ala Leu Tyr
85 90 95
Gln Val Leu Asn Lys Trp Thr Leu Gly Gln val Thr Cys Asp Leu Phe
100 105 110
Ile Ala Leu Asp Val Leu Cys Cys Thr Ser Ser Ile Leu His Leu Cys
115 120 125
Ala Ile Ala Leu Asp Arg Tyr Trp Ala Ile Thr Asp Pro Ile Asp Tyr
130 135 140
val Asn Lys Arg Thr Pro Arg Arg Ala Ala Leu Ile Ser Leu Thr
145 150 155 160
Trp Leu Ile Gly Phe Leu Ile Ser Ile Pro Pro Met Leu Gly Trp Arg
165 170 175
Thr Pro Glu Asp Arg Ser Asp Pro Asp Ala Cys Thr Ile Ser Lys Asp
180 185 190
His Gly Tyr Thr Ile Tyr Ser Thr Phe Gly Ala Phe Tyr Ile Pro Leu
195 200 205
Leu Leu Met Leu Val Leu Tyr Gly Arg Ile Phe Arg Ala Ala Arg Phe
210 215 220
Arg Ile Arg Lys Thr Val Lys Lys Val Glu Lys Thr Gly Ala Asp Thr
225 230 235 240
Arg His Gly Ala Ser Pro Ala Pro Gln Pro Lys Lys Ser Val Asn Gly
245 250 255
Glu Ser Gly Ser Arg Asn Trp Arg Leu Gly Val Glu Ser Lys Ala Gly
260 265 270
Gly Ala Leu Cys Ala Asn Gly Ala Val Arg Gln Gly Asp Asp Gly Ala
275 280 285
Ala Leu Glu Val Ile Glu Val His Arg Val Gly Asn Ser Lys Glu His
290 295 300
Leu Pro Leu Pro Ser Glu Ala Gly Pro Thr Pro Cys Ala Pro Ala Ser
305 310 315 320
Phe Glu Arg Lys Asn Glu Arg Asn Ala Glu Ala Lys Arg Lys Met Ala
325 330 335
Leu Ala Arg Glu Arg Lys Thr Val Lys Thr Leu Gly Ile Ile Met Gly
340 345 350
Thr Phe Ile Leu Cys Trp Leu Pro Phe Phe Ile Val Ala Leu Val Leu
355 360 365
Pro Phe Cys Glu Ser Ser Cys His Met Pro Thr Leu Leu Gly Ala Ile

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370	375	380
Ile Asn Trp Leu Gly Tyr Ser Asn Ser Leu Leu Asn Pro Val Ile Tyr	390	395
385		400
Ala Tyr Phe Asn Lys Asp Phe Gln Asn Ala Phe Lys Lys Ile Ile Lys	405	410
		415
Cys Asn Phe Cys Ala Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly		
	420	425
Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp	435	440
		445
Thr Ser Ser		
	450	

<210> 58

<211> 394

<212> PRT

<213> Artificial Sequence

<220>

<223> beta3AR-V2R chimera

<400> 58

Met Ala Pro Trp Pro His Glu Asn Ser Ser Leu Ala Pro Trp Pro Asp	1	5	10	15
Leu Pro Thr Leu Ala Pro Asn Thr Ala Asn Thr Ser Gly Leu Pro Gly	20	25	30	
Val Pro Trp Glu Ala Ala Leu Ala Gly Ala Leu Leu Ala Leu Ala Val	35	40	45	
Leu Ala Thr Val Gly Gly Asn Leu Leu Val Ile Val Ala Ile Ala Trp	50	55	60	
Thr Pro Arg Leu Gln Thr Met Thr Asn Val Phe Val Thr Ser Leu Ala	65	70	75	80
Ala Ala Asp Leu Val Met Gly Leu Leu Val Val Pro Pro Ala Ala Thr	85		90	95
Leu Ala Leu Thr Gly His Trp Pro Leu Gly Ala Thr Gly Cys Glu Leu	100		105	110
Trp Thr Ser Val Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu	115		120	125
Cys Ala Leu Ala Val Asp Arg Tyr Leu Ala Val Thr Asn Pro Leu Arg	130		135	140
Tyr Gly Ala Leu Val Thr Lys Arg Cys Ala Arg Thr Ala Val Val Leu	145		150	155
Val Trp Val Val Ser Ala Ala Val Ser Phe Ala Pro Ile Met Ser Gln	165		170	175
Trp Trp Arg Val Gly Ala Asp Ala Glu Ala Gln Arg Cys His Ser Asn	180		185	190
Pro Arg Cys Cys Ala Phe Ala Ser Asn Met Pro Tyr Val Leu Leu Ser	195		200	205
Ser Ser Val Ser Phe Tyr Leu Pro Leu Leu Val Met Leu Phe Val Tyr	210		215	220
Ala Arg Val Phe Val Val Ala Thr Arg Gln Leu Arg Leu Leu Arg Gly	225		230	235
Glu Leu Gly Arg Phe Pro Pro Glu Glu Ser Pro Pro Ala Pro Ser Arg	240			240
Ser Leu Ala Pro Ala Pro Val Gly Thr Cys Ala Pro Pro Glu Gly Val	245		250	255
Pro Ala Cys Gly Arg Arg Pro Ala Arg Leu Leu Pro Leu Arg Glu His	260		265	270
Arg Ala Leu Cys Thr Leu Gly Leu Ile Met Gly Thr Phe Thr Leu Cys	275		280	285
Trp Leu Pro Phe Phe Leu Ala Asn Val Leu Arg Ala Leu Gly Gly Pro	290		295	300
Ser Leu Val Pro Gly Pro Ala Phe Leu Ala Leu Asn Trp Leu Gly Tyr	305		310	315
				320

325	330	335
Ala Asn Ser Ala Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe		
340	345	350
Arg Ser Ala Phe Arg Arg Leu Leu Cys Arg Cys Ala Ala Ala Arg Gly		
355	360	365
Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala		
370	375	380
Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser		
385	390	

<210> 59
<211> 362
<212> PRT
<213> Artificial Sequence

<220>
<223> Edg1R-V2R chimera

<400> 59
Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser Ser Val
1 5 10 15
Ser Asp Tyr Val Asn Tyr Asp Ile Ile Val Arg His Tyr Asn Tyr Thr
20 25 30
Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu Thr
35 40 45
Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn Ile
50 55 60
Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro Met
65 70 75 80
Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly Val
85 90 95
Ala Tyr Thr Ala Asn Leu Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu
100 105 110
Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala Leu
115 120 125
Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile
130 135 140
Thr Met Leu Lys Met Lys Leu His Asn Gly Ser Asn Asn Phe Arg Leu
145 150 155 160
Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile Leu Gly Gly
165 170 175
Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser Ser Cys Ser
180 185 190
Thr Val Leu Pro Leu Tyr His Lys His Tyr Ile Leu Phe Cys Thr Thr
195 200 205
Val Phe Thr Leu Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg Ile
210 215 220
Tyr Ser Leu Val Arg Thr Arg Ser Arg Arg Leu Thr Phe Arg Lys Asn
225 230 235 240
Ile Ser Lys Ala Ser Arg Ser Ser Glu Lys Ser Leu Ala Leu Leu Lys
245 250 255
Thr Val Ile Ile Val Leu Ser Val Phe Ile Ala Cys Trp Ala Pro Leu
260 265 270
Phe Ile Leu Leu Leu Leu Asp Val Gly Cys Lys Val Lys Thr Cys Asp
275 280 285
Ile Leu Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala Val Leu Asn Ser
290 295 300
Gly Thr Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg Arg
305 310 315 320
Ala Phe Ile Arg Ile Met Ser Cys Cys Lys Cys Ala Ala Ala Arg Gly
325 330 335
Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala

340 345 5021US_SEQ.TXT 350
Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
355 360